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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/687,911

DATE: 05/24/2001
TIME: 17:14:13

Input Set : A:\seqlist.txt
Output Set: C:\CRF3\05242001\I687911.raw

ENTERED

```
 4 <110> APPLICANT: Rostyslav Stoika (Inventor)
 5       Gregory A. Horwitz (Inventor)
 6       Xun Zhang (Inventor)
 7       Shlomo Melmed (Inventor)
12 <120> TITLE OF INVENTION: MODULATING ACTIVATION OF LYMPHOCYTES AND
13       SCREENING POTENTIAL IMMUNOMODULATING AGENTS BY TARGETING
14       PITUITARY TUMOR TRANSFORMING GENE (PTTG) EXPRESSION AND/OR
15       FUNCTION
17 <130> FILE REFERENCE: CEDAR-44649
19 <140> CURRENT APPLICATION NUMBER: 09/687,911
20 <141> CURRENT FILING DATE: 2000-10-13
22 <150> PRIOR APPLICATION NUMBER: 09/569,956
23 <151> PRIOR FILING DATE: 2000-05-12
25 <150> PRIOR APPLICATION NUMBER: 08/894,251
26 <151> PRIOR FILING DATE: 1999-07-23
28 <150> PRIOR APPLICATION NUMBER: PCT/US86/21463
29 <151> PRIOR FILING DATE: 1997-11-21
31 <150> PRIOR APPLICATION NUMBER: 60/031,338
32 <151> PRIOR FILING DATE: 1996-11-21
34 <160> NUMBER OF SEQ ID NOS: 19
36 <170> SOFTWARE: FastSEQ for Windows Version 4.0
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 974
40 <212> TYPE: DNA
41 <213> ORGANISM: Rattus rattus
43 <400> SEQUENCE: 1
44 aattcggcac gagccaacct tgagcatctg atcctcttgg cttctccttc ctatcgctga 60
45 gctggtaggc tggagacagt tgtttgggtg ccaacatcaa caaacgattt ctgtagttta 120
46 gcgtttatga ccctggcgtg aagatttaag gtctggatta agcctgttga cttctccagc 180
47 tacttctaaa tttttgtgca taggtgctct ggtctctgtt gctgcttagt tcttccagcc 240
48 ttcctcaatg ccagttttat aatatgcagg tctctcccct cagtaatcca ggatggctac 300
49 tctgatcttt gttgataagg ataacgaaga gccaggcagc cgtttggcat ctaaggatgg 360
50 attgaagctg ggctctggtg tcaaagcctt agatgggaaa ttgcaggttt caacgccacg 420
51 agtcggcaaa gtgttcggtg ccccaggctt gcctaaagcc agcaggaagg ctctgggaac 480
52 tgtcaacaga gttactgaaa agccagtgaa gagtagtaaa cccctgcaat cgaaacagcc 540
53 gactctgagt gtgaaaaaga tcaccgagaa gtctactaag acacaaggct ctgctcctgc 600
54 tcctgatgat gcctacccag aaatagaaaa gttcttcccc ttcgatcctc tagattttga 660
55 gagttttgac ctgcctgaag agcaccagat ctcacttctc cccttgaatg gagtgcctct 720
56 catgatcctg aatgaagaga ggggggcttga gaagctgctg cacctggacc cccttcccc 780
57 tctgcagaag cccttcctac cgtgggaatc tgatccgttg ccgtctcctc ccagcgccct 840
58 ctccgctctg gatgttgaat tgccgcctgt ttgttacgat gcagatattt aaacgtctta 900
59 ctcctttata gtttatgtaa gttgtattaa taaagcattt gtgtgtaaaa aaaaaaaaa 960
60 aaactcgaga gtac                                                  974
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 199
64 <212> TYPE: PRT
65 <213> ORGANISM: Rattus rattus
```

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67 <400> SEQUENCE: 2
68 Met Ala Thr Leu Ile Phe Val Asp Lys Asp Asn Glu Glu Pro Gly Ser
69 1               5                  10                  15
70 Arg Leu Ala Ser Lys Asp Gly Leu Lys Leu Gly Ser Gly Val Lys Ala
71             20                  25                  30
72 Leu Asp Gly Lys Leu Gln Val Ser Thr Pro Arg Val Gly Lys Val Phe
73         35                  40                  45
74 Gly Ala Pro Gly Leu Pro Lys Ala Ser Arg Lys Ala Leu Gly Thr Val
75     50                  55                  60
76 Asn Arg Val Thr Glu Lys Pro Val Lys Ser Ser Lys Pro Leu Gln Ser
77 65                  70                  75                  80
78 Lys Gln Pro Thr Leu Ser Val Lys Lys Ile Thr Glu Lys Ser Thr Lys
79                 85                  90                  95
80 Thr Gln Gly Ser Ala Pro Ala Pro Asp Asp Ala Tyr Pro Glu Ile Glu
81             100                 105                 110
82 Lys Phe Phe Pro Phe Asp Pro Leu Asp Phe Glu Ser Phe Asp Leu Pro
83         115                 120                 125
84 Glu Glu His Gln Ile Ser Leu Leu Pro Leu Asn Gly Val Pro Leu Met
85     130                 135                 140
86 Ile Leu Asn Glu Glu Arg Gly Leu Glu Lys Leu Leu His Leu Asp Pro
87 145                 150                 155                 160
88 Pro Ser Pro Leu Gln Lys Pro Phe Leu Pro Trp Glu Ser Asp Pro Leu
89                 165                 170                 175
90 Pro Ser Pro Pro Ser Ala Leu Ser Ala Leu Asp Val Glu Leu Pro Pro
91             180                 185                 190
92 Val Cys Tyr Asp Ala Asp Ile
93         195
96 <210> SEQ ID NO: 3
97 <211> LENGTH: 779
98 <212> TYPE: DNA
99 <213> ORGANISM: Homo sapiens
101 <400> SEQUENCE: 3
102 atggccgcga gttgtggttt aaaccaggag tgccgcgcgt ccgttcaccg cggcctcaga 60
103 tgaatgcggc tgttaagacc tgcaataatc cagaatggct actctgatct atgttgataa 120
104 ggaaaatgga gaaccaggca cccgtgtggt tgctaaggat gggctgaagc tggggtctgg 180
105 accttcaatc aaagccttag atgggagatc tcaagtttca acaccacgtt ttggcaaaac 240
106 gttcgatgcc ccaccagcct tacctaaagc tactagaaag gctttgggaa ctgtcaacag 300
107 agctacagaa aagtctgtaa agaccaaggg accccctcaaa caaaaacagc caagctttc 360
108 tgccaaaaag atgactgaga agactgttaa agcaaaaagc tctgttcctg cctcagatga 420
109 tgcctatcca gaaatagaaa aattctttcc cttcaatcct ctagactttg agagttttga 480
110 cctgcctgaa gagcaccaga ttgcgcacct ccccttgagt ggagtgcctc tcatgatcct 540
111 tgacgaggag agagagcttg aaaagctgtt tcagctgggc ccccctcac ctgtgaagat 600
112 gccctctcca ccatgggaat ccaatctgtt gcagtctcct tcaagcattc tgtcgaccct 660
113 ggatgttgaa ttgccacctg tttgctgtga catagatatt taaatttctt agtgcttcag 720
114 agtttgtgtg tatttgtatt aataaagcat tctttaacag ataaaaaaaa aaaaaaaaa 779
116 <210> SEQ ID NO: 4
117 <211> LENGTH: 202
118 <212> TYPE: PRT
119 <213> ORGANISM: Homo sapiens
```

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```
121 <400> SEQUENCE: 4
122 Met Ala Thr Leu Ile Tyr Val Asp Lys Glu Asn Gly Glu Pro Gly Thr
123 1               5                   10                  15
124 Arg Val Val Ala Lys Asp Gly Leu Lys Leu Gly Ser Gly Pro Ser Ile
125             20                  25                  30
126 Lys Ala Leu Asp Gly Arg Ser Gln Val Ser Thr Pro Arg Phe Gly Lys
127         35                  40                  45
128 Thr Phe Asp Ala Pro Pro Ala Leu Pro Lys Ala Thr Arg Lys Ala Leu
129     50                  55                  60
130 Gly Thr Val Asn Arg Ala Thr Glu Lys Ser Val Lys Thr Lys Gly Pro
131 65                  70                  75                  80
132 Leu Lys Gln Lys Gln Pro Ser Phe Ser Ala Lys Lys Met Thr Glu Lys
133                 85                  90                  95
134 Thr Val Lys Ala Lys Ser Ser Val Pro Ala Ser Asp Asp Ala Tyr Pro
135             100                 105                 110
136 Glu Ile Glu Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Glu Ser Phe
137         115                 120                 125
138 Asp Leu Pro Glu Glu His Gln Ile Ala His Leu Pro Leu Ser Gly Val
139     130                 135                 140
140 Pro Leu Met Ile Leu Asp Glu Glu Arg Glu Leu Glu Lys Leu Phe Gln
141 145                 150                 155                 160
142 Leu Gly Pro Pro Ser Pro Val Lys Met Pro Ser Pro Pro Trp Glu Ser
143                 165                 170                 175
144 Asn Leu Leu Gln Ser Pro Ser Ser Ile Leu Ser Thr Leu Asp Val Glu
145                 180                 185                 190
146 Leu Pro Pro Val Cys Cys Asp Ile Asp Ile
147         195                 200
150 <210> SEQ ID NO: 5
151 <211> LENGTH: 31
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <223> OTHER INFORMATION: Synthetic oligonucleotide.
158 <400> SEQUENCE: 5
159 gatgctctcc gcactctggg aatccaatct g                              31
161 <210> SEQ ID NO: 6
162 <211> LENGTH: 32
163 <212> TYPE: DNA
164 <213> ORGANISM: Artificial Sequence
166 <220> FEATURE:
167 <223> OTHER INFORMATION: Synthetic oligonucleotide.
169 <400> SEQUENCE: 6
170 ttcacaagtt gaggggcgcc cagctgaaac ag                             32
172 <210> SEQ ID NO: 7
173 <211> LENGTH: 32
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Synthetic oligonucleotide specific to pCI-neo
```

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```
179       plasmid. vector.
181 <400> SEQUENCE: 7
182 ggctagagta cttaatacga ctcactatag gc                                32
184 <210> SEQ ID NO: 8
185 <211> LENGTH: 31
186 <212> TYPE: DNA
187 <213> ORGANISM: Homo sapiens
189 <400> SEQUENCE: 8
190 ctatgtcaca gcaaacaggt ggcaattcaa c                                 31
192 <210> SEQ ID NO: 9
193 <211> LENGTH: 56
194 <212> TYPE: PRT
195 <213> ORGANISM: Homo sapiens
197 <400> SEQUENCE: 9
198 Met Ile Leu Asp Glu Glu Arg Glu Leu Glu Lys Leu Phe Gln Leu Gly
199 1               5                   10                  15
200 Pro Pro Ser Pro Val Lys Met Pro Ser Pro Pro Trp Glu Ser Asn Leu
201             20                  25                  30
202 Leu Gln Ser Pro Ser Ser Ile Leu Ser Thr Leu Asp Val Glu Leu Pro
203             35                  40                  45
204 Pro Val Cys Cys Asp Ile Asp Ile
205     50                  55
208 <210> SEQ ID NO: 10
209 <211> LENGTH: 168
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
213 <400> SEQUENCE: 10
214 atgatccttg acgaggagag agagcttgaa aagctgtttc agctgggccc cccttcacct 60
215 gtgaagatgc cctctccacc atgggaatcc aatctgttgc agtctccttc aagcattctg 120
216 tcgaccctgg atgttgaatt gccacctgtt tgctgtgaca tagatatt               168
218 <210> SEQ ID NO: 11
219 <211> LENGTH: 16
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Anchored primer sequence.
226 <400> SEQUENCE: 11
227 aagcttttttt tttttg                                                 16
229 <210> SEQ ID NO: 12
230 <211> LENGTH: 13
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: Arbitrary primer sequence.
237 <400> SEQUENCE: 12
238 aagcttgctg ctc                                                     13
240 <210> SEQ ID NO: 13
241 <211> LENGTH: 16
242 <212> TYPE: DNA
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```
243 <213> ORGANISM: Artificial Sequence
245 <220> FEATURE:
246 <223> OTHER INFORMATION: n = a, g, or c; Anchored primer sequence.
248 <400> SEQUENCE: 13
```
W--> 249 aagctttttt tttttn   16
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251 <210> SEQ ID NO: 14
252 <211> LENGTH: 194
253 <212> TYPE: PRT
254 <213> ORGANISM: Mus musculus
256 <400> SEQUENCE: 14
257 Met Ala Thr Leu Ile Phe Val Asp Lys Asp Asn Glu Glu Pro Gly Arg
258  1               5                   10                  15
259 Arg Leu Ala Ser Lys Asp Gly Leu Lys Leu Gly Thr Gly Val Lys Ala
260              20                  25                  30
261 Leu Asp Gly Lys Leu Gln Val Ser Thr Pro Arg Val Gly Lys Val Phe
262          35                  40                  45
263 Asn Ala Pro Ala Val Pro Lys Ala Ser Arg Lys Ala Leu Gly Thr Val
264      50                  55                  60
265 Asn Arg Val Ala Glu Lys Pro Met Lys Thr Gly Lys Pro Leu Gln Pro
266 65                  70                  75                  80
267 Lys Gln Pro Thr Leu Thr Gly Lys Lys Ile Thr Glu Lys Ser Thr Lys
268          ·       85                  90                  95
269 Thr Gln Ser Ser Val Pro Ala Pro Asp Asp Ala Tyr Pro Glu Ile Glu
270              100                 105                 110
271 Lys Phe Phe Pro Phe Asn Pro Leu Asp Phe Asp Leu Pro Glu Glu His
272          115                 120                 125
273 Gln Ile Ser Leu Leu Pro Leu Asn Gly Val Pro Leu Ile Thr Leu Asn
274      130                 135                 140
275 Glu Glu Arg Gly Leu Glu Lys Leu Leu His Leu Gly Pro Pro Ser Pro
276 145                 150                 155                 160
277 Leu Lys Thr Pro Phe Leu Ser Trp Glu Ser Asp Pro Lys Pro Pro Ser
278              165                 170                 175
279 Ala Leu Ser Thr Leu Asp Val Glu Leu Pro Pro Val Cys Tyr Asp Ala
280              180                 185                 190
281 Asp Ile
285 <210> SEQ ID NO: 15
286 <211> LENGTH: 945
287 <212> TYPE: DNA
288 <213> ORGANISM: Mus musculus
290 <400> SEQUENCE: 15
291 tcttgaactt gttatgtagc aggaggccaa atttgagcat cctcttggct tctctttata 60
292 gcagagattg taggctggag acagttttga tgggtgccaa cataaactga tttctgtaag 120
293 agttgagtgt tttatgaccc tggcgtgcag atttaggatc tggattaagc ctgttgactt 180
294 ctccagctac ttataaattt ttgtgcatag gtgccctggg taaagcttgg tctctgttac 240
295 tgcgtagttt ttccagccgt ctcaatgcca atattcaggc tctctccctt agagtaatcc 300
296 agaatggcta ctcttatctt tgttgataag gataatgaag aacccggccg ccgtttggca 360
297 tctaaggatg ggttgaagct gggcactggt gtcaaggcct tagatgggaa attgcaggtt 420
298 tcaacgcctc gagtcggcaa agtgttcaat gctccagccg tgcctaaagc cagcagaaag 480
299 gctttgggga cagtcaacag agttgccgaa aagcctatga agactggcaa acccctccaa 540
```

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```
L:249 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:249 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
```